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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/668,314A

Input Set : A:\6280NCPseq.txt

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4 <110> APPLICANT: Gurney, Mark  
 5 Bienkowski, Michael J.  
 7 <120> TITLE OF INVENTION: ALZHEIMER'S DISEASE SECRETASE, APP SUBSTRATES THEREFOR, AND  
 USES

8 THEREOF  
 10 <130> FILE REFERENCE: 28341/6280NCP  
 12 <140> CURRENT APPLICATION NUMBER: 09/668,314A  
 13 <141> CURRENT FILING DATE: 2000-09-22  
 15 <150> PRIOR APPLICATION NUMBER: 60/169,232  
 16 <151> PRIOR FILING DATE: 1999-12-06  
 18 <150> PRIOR APPLICATION NUMBER: 09/416,901  
 19 <151> PRIOR FILING DATE: 1999-10-13  
 21 <150> PRIOR APPLICATION NUMBER: 60/155,493  
 22 <151> PRIOR FILING DATE: 1999-09-23  
 24 <150> PRIOR APPLICATION NUMBER: 09/404,133  
 25 <151> PRIOR FILING DATE: 1999-09-23  
 27 <150> PRIOR APPLICATION NUMBER: PCT/US99/20881  
 28 <151> PRIOR FILING DATE: 1999-09-23  
 30 <150> PRIOR APPLICATION NUMBER: 60/101,594  
 31 <151> PRIOR FILING DATE: 1998-09-24  
 33 <160> NUMBER OF SEQ ID NOS: 82  
 35 <170> SOFTWARE: PatentIn Ver. 2.0  
 37 <210> SEQ ID NO: 1  
 38 <211> LENGTH: 1804  
 39 <212> TYPE: DNA  
 40 <213> ORGANISM: Homo sapiens  
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 45 cgcgtagttg cggccaccccc gggaccggg accccctgccc agcgccacgc cgacggcttg 180  
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 48 ccccccgcaga agctacagat ttcgttgac actgaaagca gtaactttgc cgtggcagga 360  
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 54 caagcaaaca tccccaacgt tttctccatg cagatgtgtg gagccggcgtt gcccgttgct 720  
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66 cagtcttga gcgagcccat tttgtggatt gtgtcctatg cgctcatgag cgtctgtgga 1440
67 gccatcctcc ttgtcttaat cgtcctgctg ctgctgccgt tccggtgtca gcgtcgcccc 1500
68 cgtgaccctg aggtcgtaa tgatgagtcc tctctggtca gacatcgctg gaaatgaata 1560
69 gccaggcctg acctaagca accatgaact cagctattaa gaaaatcaca tttccagggc 1620
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71 gctcccagat gccttctaga ttcactgtct tttgattctt gattttcaag ctttcaaatac 1740
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85 20 25 30
87 Leu Arg Val Ala Ala Ala Thr Asn Arg Val Val Ala Pro Thr Pro Gly
88 35 40 45
90 Pro Gly Thr Pro Ala Glu Arg His Ala Asp Gly Leu Ala Leu Ala Leu
91 50 55 60
93 Glu Pro Ala Leu Ala Ser Pro Ala Gly Ala Ala Asn Phe Leu Ala Met
94 65 70 75 80
96 Val Asp Asn Leu Gln Gly Asp Ser Gly Arg Gly Tyr Tyr Leu Glu Met
97 85 90 95
99 Leu Ile Gly Thr Pro Pro Gln Lys Leu Gln Ile Leu Val Asp Thr Gly
100 100 105 110
102 Ser Ser Asn Phe Ala Val Ala Gly Thr Pro His Ser Tyr Ile Asp Thr
103 115 120 125
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106 130 135 140
108 Val Thr Val Lys Tyr Thr Gln Gly Ser Trp Thr Gly Phe Val Gly Glu
109 145 150 155 160
111 Asp Leu Val Thr Ile Pro Lys Gly Phe Asn Thr Ser Phe Leu Val Asn
112 165 170 175
115 Ile Ala Thr Ile Phe Glu Ser Glu Asn Phe Phe Leu Pro Gly Ile Lys
116 180 185 190
118 Trp Asn Gly Ile Leu Gly Leu Ala Tyr Ala Thr Leu Ala Lys Pro Ser
119 195 200 205
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122 210 215 220
124 Pro Asn Val Phe Ser Met Gln Met Cys Gly Ala Gly Leu Pro Val Ala
125 225 230 235 240
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129 245 250 255
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132 260 265 270

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137 Asn Leu Asp Cys Arg Glu Tyr Asn Ala Asp Lys Ala Ile Val Asp Ser
138      290          295          300
140 Gly Thr Thr Leu Leu Arg Leu Pro Gln Lys Val Phe Asp Ala Val Val
141      305          310          315          320
143 Glu Ala Val Ala Arg Ala Ser Leu Ile Pro Glu Phe Ser Asp Gly Phe
144      325          330          335
146 Trp Thr Gly Ser Gln Leu Ala Cys Trp Thr Asn Ser Glu Thr Pro Trp
147      340          345          350
149 Ser Tyr Phe Pro Lys Ile Ser Ile Tyr Leu Arg Asp Glu Asn Ser Ser
150      355          360          365
152 Arg Ser Phe Arg Ile Thr Ile Leu Pro Gln Leu Tyr Ile Gln Pro Met
153      370          375          380
155 Met Gly Ala Gly Leu Asn Tyr Glu Cys Tyr Arg Phe Gly Ile Ser Pro
156      385          390          395          400
158 Ser Thr Asn Ala Leu Val Ile Gly Ala Thr Val Met Glu Gly Phe Tyr
159      405          410          415
161 Val Ile Phe Asp Arg Ala Gln Lys Arg Val Gly Phe Ala Ala Ser Pro
162      420          425          430
164 Cys Ala Glu Ile Ala Gly Ala Ala Val Ser Glu Ile Ser Gly Pro Phe
165      435          440          445
167 Ser Thr Glu Asp Val Ala Ser Asn Cys Val Pro Ala Gln Ser Leu Ser
168      450          455          460
171 Glu Pro Ile Leu Trp Ile Val Ser Tyr Ala Leu Met Ser Val Cys Gly
172      465          470          475          480
174 Ala Ile Leu Leu Val Leu Ile Val Leu Leu Leu Pro Phe Arg Cys
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192 ctgcggctgc cccgggagac cgacgaagag cccgaggagc cccggccggag gggcagcttt 180
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200 ctggtaaagc agaccacgt tcccaacctc ttctccctgc acctttgtgg tgctggcttc 660
201 cccctcaacc agtctgaagt gctggcctt gtcggaggga gcatgatcat tggaggtatc 720

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 204 tacaactatg acaagagcat tgtggacagt ggcaccacca actttcgttt gcccaagaaa 900  
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 208 atccttcgc agcaataacct gcggccagtg gaagatgtgg ccacgtccca agacgactgt 1140  
 209 tacaagtttgc ccatctcaca gtcatccacg ggcactgtta tggagactgt tatcatggag 1200  
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 215 aagtggaggag gcccatgggc agaagataga gattccctg gaccacaccc cctgtggttca 1560  
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 236 20 25 30  
 238 Gly Leu Gly Gly Ala Pro Leu Gly Leu Arg Leu Pro Arg Glu Thr Asp  
 239 35 40 45  
 241 Glu Glu Pro Glu Glu Pro Gly Arg Arg Gly Ser Phe Val Glu Met Val  
 242 50 55 60  
 244 Asp Asn Leu Arg Gly Lys Ser Gly Gln Gly Tyr Tyr Val Glu Met Thr  
 245 65 70 75 80  
 247 Val Gly Ser Pro Pro Gln Thr Leu Asn Ile Leu Val Asp Thr Gly Ser  
 248 85 90 95  
 250 Ser Asn Phe Ala Val Gly Ala Ala Pro His Pro Phe Leu His Arg Tyr  
 251 100 105 110  
 254 Tyr Gln Arg Gln Leu Ser Ser Thr Tyr Arg Asp Leu Arg Lys Gly Val  
 255 115 120 125  
 257 Tyr Val Pro Tyr Thr Gln Gly Lys Trp Glu Gly Glu Leu Gly Thr Asp  
 258 130 135 140  
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 263 Ala Ala Ile Thr Glu Ser Asp Lys Phe Phe Ile Asn Gly Ser Asn Trp

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272	Asn Leu Phe Ser Leu His Leu Cys Gly Ala Gly Phe Pro Leu Asn Gln		
273	210	215	220
275	Ser Glu Val Leu Ala Ser Val Gly Gly Ser Met Ile Ile Gly Gly Ile		
276	225	230	235
278	240	245	250
279	Asp His Ser Leu Tyr Thr Gly Ser Leu Trp Tyr Thr Pro Ile Arg Arg		
282	255	260	265
283	Glu Trp Tyr Tyr Glu Val Ile Ile Val Arg Val Glu Ile Asn Gly Gln		
285	270	275	280
286	Asp Leu Lys Met Asp Cys Lys Glu Tyr Asn Tyr Asp Lys Ser Ile Val		
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292	Ala Val Lys Ser Ile Lys Ala Ala Ser Ser Thr Glu Lys Phe Pro Asp		
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298	Pro Trp Asn Ile Phe Pro Val Ile Ser Leu Tyr Leu Met Gly Glu Val		
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301	Thr Asn Gln Ser Phe Arg Ile Thr Ile Leu Pro Gln Gln Tyr Leu Arg		
303	355	360	365
304	Pro Val Glu Asp Val Ala Thr Ser Gln Asp Asp Cys Tyr Lys Phe Ala		
306	370	375	380
307	Ile Ser Gln Ser Ser Thr Gly Thr Val Met Gly Ala Val Ile Met Glu		
309	385	390	395
310	400	405	410
312	Gly Phe Tyr Val Val Phe Asp Arg Ala Arg Lys Arg Ile Gly Phe Ala		
313	415	420	425
315	430	435	440
316	445	450	455
318	460	465	470
319	Ala Ala		
321	475	480	485
322	Ile Cys Ala Leu Phe Met Leu Pro Leu Cys Leu Met Val Cys Gln Trp		
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VERIFICATION SUMMARY

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